



SEQUENCE LISTING

<110> Rauch, Charles
Walczak, Henning

<120> RECEPTOR THAT BINDS TRAIL

<130> 2625-E

<140> US 09/378,045

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<151> 1997-06-26

<150> US 08/869,852

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<150> US 08/829,536

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<150> US 08/815,255

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<150> US 08/799,861

<151> 1997-02-13

<160> 5

<170> PatentIn version 3.0/ Microsoft Word, Version 6.0.1

<210> 1

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<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1)..(1323)

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Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg Lys
1 5 10 15

agg cac ggc cca gga ccc agg gag gcg cgg gga gcc agg cct ggg ccc 96
Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Pro
20 25 30

cgg gtc ccc aag acc ctt gtg ctc gtt gtc gcc gcg gtc ctg ctg ttg 144
Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu
35 40 45

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MAY 02 2001

TECH CENTER 1600/2000

Sub
D1

B1

gtc tca gct gag tct gct ctg atc acc caa caa gac cta gct ccc cag	192
Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln	
50 55 60	
cag aga gcg gcc cca caa caa aag agg tcc agc ccc tca gag gga ttg	240
Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu	
65 70 75 80	
tgt cca cct gga cac cat atc tca gaa gac ggt aga gat tgc atc tcc	288
Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser	
85 90 95	
tgc aaa tat gga cag gac tat agc act cac tgg aat gac ctc ctt ttc	336
Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe	
100 105 110	
tgc ttg cgc tgc acc agg tgt gat tca ggt gaa gtg gag cta agt ccg	384
Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro	
115 120 125	
tgc acc acg acc aga aac aca gtg tgt cag tgc gaa gaa ggc acc ttc	432
Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe	
130 135 140	
cgg gaa gaa gat tct cct gag atg tgc cgg aag tgc cgc aca ggg tgt	480
Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys	
145 150 155 160	
ccc aga ggg atg gtc aag gtc ggt gat tgt aca ccc tgg agt gac atc	528
Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile	
165 170 175	
gaa tgt gtc cac aaa gaa tca ggt aca aag cac agt ggg gaa gcc cca	576
Glu Cys Val His Lys Glu Ser Gly Thr Lys His Ser Gly Glu Ala Pro	
180 185 190	
gct gtg gag gag acg gtg acc tcc agc cca ggg act cct gcc tct ccc	624
Ala Val Glu Glu Thr Val Thr Ser Ser Pro Gly Thr Pro Ala Ser Pro	
195 200 205	
tgt tct ctc tca ggc atc atc ata gga gtc aca gtt gca gcc gta gtc	672
Cys Ser Leu Ser Gly Ile Ile Ile Gly Val Thr Val Ala Ala Val Val	
210 215 220	
ttg att gtg gct gtg ttt gtt tgc aag tct tta ctg tgg aag aaa gtc	720
Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys Val	
225 230 235 240	
ctt cct tac ctg aaa ggc atc tgc tca ggt ggt ggt ggg gac cct gag	768
Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly Asp Pro Glu	
245 250 255	
cgt gtg gac aga agc tca caa cga cct ggg gct gag gac aat gtc ctc	816
Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp Asn Val Leu	
260 265 270	
aat gag atc gtg agt atc ttg cag ccc acc cag gtc cct gag cag gaa	864
Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro Glu Gln Glu	
275 280 285	

Sub
DI
Cont

atg gaa gtc cag gag cca gca gag cca aca ggt gtc aac atg ttg tcc	912
Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn Met Leu Ser	
290 295 300	
ccc ggg gag tca gag cat ctg ctg gaa ccg gca gaa gct gaa agg tct	960
Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala Glu Arg Ser	
305 310 315 320	
cag agg agg agg ctg ctg gtt cca gca aat gaa ggt gat ccc act gag	1008
Gln Arg Arg Arg Leu Leu Val Pro Ala Asn Glu Gly Asp Pro Thr Glu	
325 330 335	
act ctg aga cag tgc ttc gat gac ttt gca gac ttg gtg ccc ttt gac	1056
Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val Pro Phe Asp	
340 345 350	
tcc tgg gag ccg ctc atg agg aag ttg ggc ctc atg gac aat gag ata	1104
Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu Ile	
355 360 365	
aag gtg gct aaa gct gag gca gcg ggc cac agg gac acc ttg tac acg	1152
Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu Tyr Thr	
370 375 380	
atg ctg ata aag tgg gtc aac aaa acc ggg cga gat gcc tct gtc cac	1200
Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala Ser Val His	
385 390 395 400	
acc ctg ctg gat gcc ttg gag acg ctg gga gag aga ctt gcc aag cag	1248
Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln	
405 410 415	
aag att gag gac cac ttg ttg agc tct gga aag ttc atg tat cta gaa	1296
Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu	
420 425 430	
ggt aat gca gac tct gcc atg tcc taa	1323
Gly Asn Ala Asp Ser Ala Met Ser	
435 440	

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 <213> Homo sapiens

<400> 2

Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg Lys	
1 5 10 15	
Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Pro	
20 25 30	
Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu	
35 40 45	
Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln	
50 55 60	

Gln	Arg	Ala	Ala	Pro	Gln	Gln	Lys	Arg	Ser	Ser	Pro	Ser	Glu	Gly	Leu	65	70	75	80
Cys	Pro	Pro	Gly	His	His	Ile	Ser	Glu	Asp	Gly	Arg	Asp	Cys	Ile	Ser	85	90	95	
Cys	Lys	Tyr	Gly	Gln	Asp	Tyr	Ser	Thr	His	Trp	Asn	Asp	Leu	Leu	Phe	100	105	110	
Cys	Leu	Arg	Cys	Thr	Arg	Cys	Asp	Ser	Gly	Glu	Val	Glu	Leu	Ser	Pro	115	120	125	
Cys	Thr	Thr	Thr	Arg	Asn	Thr	Val	Cys	Gln	Cys	Glu	Glu	Gly	Thr	Phe	130	135	140	
Arg	Glu	Glu	Asp	Ser	Pro	Glu	Met	Cys	Arg	Lys	Cys	Arg	Thr	Gly	Cys	145	150	155	160
Pro	Arg	Gly	Met	Val	Lys	Val	Gly	Asp	Cys	Thr	Pro	Trp	Ser	Asp	Ile	165	170	175	
Glu	Cys	Val	His	Lys	Glu	Ser	Gly	Thr	Lys	His	Ser	Gly	Glu	Ala	Pro	180	185	190	
Ala	Val	Glu	Glu	Thr	Val	Thr	Ser	Ser	Pro	Gly	Thr	Pro	Ala	Ser	Pro	195	200	205	
Cys	Ser	Leu	Ser	Gly	Ile	Ile	Ile	Gly	Val	Thr	Val	Ala	Ala	Val	Val	210	215	220	
Leu	Ile	Val	Ala	Val	Phe	Val	Cys	Lys	Ser	Leu	Leu	Trp	Lys	Lys	Val	225	230	235	240
Leu	Pro	Tyr	Leu	Lys	Gly	Ile	Cys	Ser	Gly	Gly	Gly	Gly	Asp	Pro	Glu	245	250	255	
Arg	Val	Asp	Arg	Ser	Ser	Gln	Arg	Pro	Gly	Ala	Glu	Asp	Asn	Val	Leu	260	265	270	
Asn	Glu	Ile	Val	Ser	Ile	Leu	Gln	Pro	Thr	Gln	Val	Pro	Glu	Gln	Glu	275	280	285	
Met	Glu	Val	Gln	Glu	Pro	Ala	Glu	Pro	Thr	Gly	Val	Asn	Met	Leu	Ser	290	295	300	
Pro	Gly	Glu	Ser	Glu	His	Leu	Leu	Glu	Pro	Ala	Glu	Ala	Glu	Arg	Ser	305	310	315	320
Gln	Arg	Arg	Arg	Leu	Leu	Val	Pro	Ala	Asn	Glu	Gly	Asp	Pro	Thr	Glu	325	330	335	
Thr	Leu	Arg	Gln	Cys	Phe	Asp	Asp	Phe	Ala	Asp	Leu	Val	Pro	Phe	Asp	340	345	350	
Ser	Trp	Glu	Pro	Leu	Met	Arg	Lys	Leu	Gly	Leu	Met	Asp	Asn	Glu	Ile	355	360	365	
Lys	Val	Ala	Lys	Ala	Glu	Ala	Ala	Gly	His	Arg	Asp	Thr	Leu	Tyr	Thr	370	375	380	

Sub
DI
cont

Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala Ser Val His
385 390 395 400

Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln
405 410 415

Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu
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Gly Asn Ala Asp Ser Ala Met Ser
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<210> 3
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ttt gac tcc tgg gag ccg ctc atg agg aag ttg ggc ctc atg gac aat 95
Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp Asn
20 25 30

gag ata aag gtg gct aaa gct gag gca gcg ggc cac agg gac acc ttg 143
Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu
35 40 45

tnc acn atg ctg at 157
Xaa Thr Met Leu
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<213> Homo sapiens

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Sub
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Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val Pro Phe
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Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu
20 25 30

Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu Xaa
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Thr Met Leu
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<210> 5
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<213> Artificial

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<223> FLAG peptide

<400> 5

Asp Tyr Lys Asp Asp Asp Asp Lys
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Sub
DI
Cont

B1
Cont